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RAW SEQUENCE LISTING

DATE: 11/06/2001

PATENT APPLICATION: US/09/931,157

TIME: 11:56:06

Input Set : A:\299002032411.txt

Output Set: N:\CRF3\11062001\I931157.raw

4 <110> APPLICANT: Imura, Hiroo
 5 Nakao, Kazuwa
 6 Nakanishi, Shigetada
 8 <120> TITLE OF INVENTION: Human Endothelin Receptor
 11 <130> FILE REFERENCE: 299002032411
 13 <140> CURRENT APPLICATION NUMBER: 09/931,157
 C--> 14 <141> CURRENT FILING DATE: 2001-10-15 8/27
 16 <150> PRIOR APPLICATION NUMBER: 08/121,446
 17 <151> PRIOR FILING DATE: 1993-09-14
 19 <150> PRIOR APPLICATION NUMBER: 07/911,684
 20 <151> PRIOR FILING DATE: 1992-07-10
 22 <150> PRIOR APPLICATION NUMBER: JP 3-172828
 23 <151> PRIOR FILING DATE: 1991-07-12
 25 <160> NUMBER OF SEQ ID NOS: 2
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 4105
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo Sapiens
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 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (485)...(1768)
 38 <221> NAME/KEY: sig_peptide
 39 <222> LOCATION: (485)...(544)
 41 <221> NAME/KEY: mat_peptide
 42 <222> LOCATION: (545)...(1768)
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 47 cgcgcgcgcg tacagtcata ccgctggtct gacgattgtg gagaggcggg ggagaggctt 180
 48 catccatccc acccggtcgt cgcgggggat tgggggtcca gcgacacctc cccggggagaa 240
 49 gcagtgcaca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgcgcgcg 300
 50 cggagcccg gacaccggcc accctccgcg ccacccacct tcgctttctc cggttctctc 360
 51 tggcccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
 52 aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttctct aaatttgctt 480
 53 caag atg gaa acc ctt tgc ctg agg gca tcc ttt tgg ctg gca ctg gtt 529
 54 Met Glu Thr Leu Cys Leu Arg Ala Ser Phe Trp Leu Ala Leu Val
 55 -20 -15 -10
 57 gga tgt gta atc agt gat aat cct gag aga tac agc aca aat cta agc 577
 58 Gly Cys Val Ile Ser Asp Asn Pro Glu Arg Tyr Ser Thr Asn Leu Ser
 59 -5 1 5 10
 61 aat cat gtg gat gat ttc acc act ttt cgt ggc aca gag ctg agc ttc 625
 62 Asn His Val Asp Phe Thr Thr Phe Arg Gly Thr Glu Leu Ser Phe
 63 15 20 25
 65 ctg gtt acc act cat caa ccc act aat ttg gtc cta ccc agc aat ggc 673
 66 Leu Val Thr Thr His Gln Pro Thr Asn Leu Val Leu Pro Ser Asn Gly
 67 30 35 40

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69	tca atg cac aac tat tgc cca cag cag act aaa att act tca gct ttc	721
70	Ser Met His Asn Tyr Cys Pro Gln Gln Thr Lys Ile Thr Ser Ala Phe	
71	45 50 55	
73	aaa tac att aac act gtg ata tct tgt act att ttc atc gtg gga atg	769
74	Lys Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met	
75	60 65 70 75	
77	gtg ggg aat gca act ctg ctc agg atc att tac cag aac aaa tgt atg	817
78	Val Gly Asn Ala Thr Leu Leu Arg Ile Ile Tyr Gln Asn Lys Cys Met	
79	80 85 90	
81	agg aat ggc ccc aac gcg ctg ata gcc agt ctt gcc ctt gga gac ctt	865
82	Arg Asn Gly Pro Asn Ala Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu	
83	95 100 105	
85	atc tat gtg gtc att gat ctc cct atc aat gta ttt aag ctg ctg gct	913
86	Ile Tyr Val Val Ile Asp Leu Pro Ile Asn Val Phe Lys Leu Leu Ala	
87	110 115 120	
89	ggg cgc tgg cct ttt gat cac aat gac ttt ggc gta ttt ctt tgc aag	961
90	Gly Arg Trp Pro Phe Asp His Asn Asp Phe Gly Val Phe Leu Cys Lys	
91	125 130 135	
93	ctg ttc ccc ttt ttg cag aag tcc tcg gtg ggg atc acc gtc ctc aac	1009
94	Leu Phe Pro Phe Leu Gln Lys Ser Ser Val Gly Ile Thr Val Leu Asn	
95	140 145 150 155	
97	ctc tgc gct ctt agt gtt gac agg tac aga gca gtt gcc tcc tgg agt	1057
98	Leu Cys Ala Leu Ser Val Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser	
99	160 165 170	
101	cgt gtt cag gga att ggg att cct ttg gta act gcc att gaa att gtc	1105
102	Arg Val Gln Gly Ile Gly Ile Pro Leu Val Thr Ala Ile Glu Ile Val	
103	175 180 185	
105	tcc atc tgg atc ctg tcc ttt atc ctg gcc att cct gaa gcg att ggc	1153
106	Ser Ile Trp Ile Leu Ser Phe Ile Leu Ala Ile Pro Glu Ala Ile Gly	
107	190 195 200	
109	ttc gtc atg gta ccc ttt gaa tat agg ggt gaa cag cat aaa acc tgt	1201
110	Phe Val Met Val Pro Phe Glu Tyr Arg Gly Glu Gln His Lys Thr Cys	
111	205 210 215	
113	atg ctc aat gcc aca tca aaa ttc atg gag ttc tac caa gat gta aag	1249
114	Met Leu Asn Ala Thr Ser Lys Phe Met Glu Phe Tyr Gln Asp Val Lys	
115	220 225 230 235	
117	gac tgg tgg ctc ttc ggg ttc tat ttc tgt atg ccc ttg gtg tgc act	1297
118	Asp Trp Trp Leu Phe Gly Phe Tyr Phe Cys Met Pro Leu Val Cys Thr	
119	240 245 250	
121	gcg atc ttc tac acc ctc atg act tgt gag atg ttg aac aga agg aat	1345
122	Ala Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn Arg Arg Asn	
123	255 260 265	
125	ggc agc ttg aga att gcc ctc agt gaa cat ctt aag cag cgt cga gaa	1393
126	Gly Ser Leu Arg Ile Ala Leu Ser Glu His Leu Lys Gln Arg Arg Glu	
127	270 275 280	
129	gtg gca aaa aca gtt ttc tgc ttg gtt gta att ttt gct ctt tgc tgg	1441
130	Val Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala Leu Cys Trp	
131	285 290 295	
133	ttc cct ctt cac tta agc cgt ata ttg aag aaa act gtg tat aac gaa	1489

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134 Phe Pro Leu His Leu Ser Arg Ile Leu Lys Lys Thr Val Tyr Asn Glu
135 300                               305                               310                               315
137 atg gac aag aac cga tgt gaa tta ctt agt ttc tta ctg ctc atg gat      1537
138 Met Asp Lys Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Leu Met Asp
139                               320                               325                               330
141 tac atc ggt att aac ttg gca acc atg aat tca tgt ata aac ccc ata      1585
142 Tyr Ile Gly Ile Asn Leu Ala Thr Met Asn Ser Cys Ile Asn Pro Ile
143                               335                               340                               345
145 gct ctg tat ttt gtg agc aag aaa ttt aaa aat tgt ttc cag tca tgc      1633
146 Ala Leu Tyr Phe Val Ser Lys Lys Phe Lys Asn Cys Phe Gln Ser Cys
147                               350                               355                               360
149 ctc tgc tgc tgc tgt tac cag tcc aaa agt ctg atg acc tcg gtc ccc      1681
150 Leu Cys Cys Cys Cys Tyr Gln Ser Lys Ser Leu Met Thr Ser Val Pro
151                               365                               370                               375
153 atg aac gga aca agc atc cag tgg aag aac cac gat caa aac aac cac      1729
154 Met Asn Gly Thr Ser Ile Gln Trp Lys Asn His Asp Gln Asn Asn His
155 380                               385                               390                               395
157 aac aca gac cgg agc agc cat aag gac agc atg aac tga ccacccttag      1778
158 Asn Thr Asp Arg Ser Ser His Lys Asp Ser Met Asn *
159                               400                               405
161 aagcactcct cggtaactccc ataatcctct cggagaaaaa aatcacaagg caactgtgac      1838
162 tccgggaatc tcttctctga tcttctctoc ttaattcact cccacaccca agaagaaatg      1898
163 ctttccaaaa ccgcaaggta gactgggttta tccaccacaca acatctacga atcgtacttc      1958
164 tttaattgat ctaattttaca tattctgcgt gttgtattca gcactaaaaa atgggtgggag      2018
165 ctggggggaga atgaagactg ttaaagtaaa ccagaaggat atttactact tttgcatgaa      2078
166 aatagagctt tcaagtacat ggctagcttt tatggcagtt ctggtgaatg ttcaatggga      2138
167 actggtcacc atgaaacttt agagattaac gacaagattt tctacttttt ttaagtgatt      2198
168 ttttgccttt cagccaaaca caatatgggc tcagggtcact tttatttgaa atgtcatttg      2258
169 gtgccagtat tttttaactg cataatagcc taacatgatt atttgaactt atttacacat      2318
170 agtttgaaaa aaaaaagaca aaaatagtat tcagggtgagc aattagatta gtattttcca      2378
171 cgtcactatt tatttttttta aaacacaaat tctaaagcta caacaaatac tacaggccct      2438
172 taaagcacag tctgatgaca catttggcag tttaatatagat gttactcaaa gaatttttta      2498
173 agaactgtat tttatttttt aaatgggtgt ttattacaag ggaccttgaa catgttttgt      2558
174 atgttaaatt caaaagtaat gtttcaatca gatagttctt tttcacaagt tcaatactgt      2618
175 ttttcatgta aattttgtat gaaaaatcaa tgtcaagtac caaaatgtta atgtatgtgt      2678
176 catttaactc tgccctgagac tttcagtgca ctgtatatag aagtctaaaa cacacctaag      2738
177 agaaaaagat cgaatttttc agatgattcg gaaattttca ttcagggtatt tgtaatatgt      2798
178 acatatatat gtatatacat atcacctcct attctcttaa tttttgttaa aatgttaact      2858
179 ggcagtaagt cttttttgat cattcccttt tccatatagg aaacataatt ttgaagtggc      2918
180 cagatgagtt tatcatgtca gtgaaaaata attaccacaca aatgccacca gtaacttaac      2978
181 gattcttcac ttcttggggt tttcagtatg aacctaaact cccaccccaa catctccctc      3038
182 ccacattgtc accatttcaa agggccacaca gtgacttttg ctgggcattt tcccagatgt      3098
183 ttacagactg tgagtacagc agaaaatctt ttactagtgt gtgtgtgtat atatataaac      3158
184 aattgtaaat ttcttttagc ccatttttct agactgtctc tgtggaatat atttgtgtgt      3218
185 gtgatatatg catgtgtgtg atggtatgta tggatttaat ctaatctaata aattgtgccc      3278
186 cgcagttgtg ccaaagtgca tagtctgagc taaaatctag gtgattgttc atcatgacaa      3338
187 cctgcctcag tccattttta cctgtagcaa ccttctgcat tcataaatct tgtaatcatg      3398
188 ttaccattac aaatgggata taagaggcag cgtgaaagca gatgagctgt ggactagcaa      3458
189 tatagggttt tgtttggttg gttggtttga taaagcagta tttgggttca tattgtttcc      3518

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190 tgtgctggag caaaagtcac tacactttga agtattatat tgttcttata ctcaattcaa 3578
191 tgtggtgatg aaattgccag gttgtctgat atttctttca gacttcgcca gacagattgc 3638
192 tgataataaa ttaggtaaga taatttggtg ggccatattt taggacaggt aaaataacat 3698
193 caggttccag ttgcttgaat tgcaaggcta agaagtactg cccttttgtg tgttagcagt 3758
194 caaatctatt attccactgg cgcacatata gcagtgatat atgcctataa tataagccat 3818
195 aggttcacac cattttgttt agacaattgt ctttttttca agatgctttg tttctttcat 3878
196 atgaaaaaaaa tgcattttat aaattcagaa agtcatagat ttctgaaggc gtcaacgtgc 3938
197 attttattta tggactggta agtaactgtg gtttactagc aggaatattt ccaattttcta 3998
198 cctttactac atcttttcaa caagtaactt tgtagaaatg agccagaagc caaggccctg 4058
199 agttggcagt ggcccataag tgtaaaataa aagtttacag aaacctt 4105
201 <210> SEQ ID NO: 2
202 <211> LENGTH: 4301
203 <212> TYPE: DNA
204 <213> ORGANISM: Homo Sapiens
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (238)...(1566)
210 <400> SEQUENCE: 2
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212 aggtaggcat ttgcccgggt gggacgcctt gccagagcag tgtgtggcag gccccgtgg 120
213 aggatcaaca cagtggctga acactgggaa ggaactggta cttggagtct ggacatctga 180
214 aacttggctc tgaaactgcg gagcggccac cggacgcctt ctggagcagg tagcagc atg 240
215 Met
216 1
218 cag ccg cct cca agt ctg tgc gga cgc gcc ctg gtt gcg ctg gtt ctt 288
219 Gln Pro Pro Pro Ser Leu Cys Gly Arg Ala Leu Val Ala Leu Val Leu
220 5 10 15
222 gcc tgc ggc ctg tcg cgg atc tgg gga gag gag aga ggc ttc ccg cct 336
223 Ala Cys Gly Leu Ser Arg Ile Trp Gly Glu Glu Arg Gly Phe Pro Pro
224 20 25 30
226 gac agg gcc act ccg ctt ttg caa acc gca gag ata atg acg cca ccc 384
227 Asp Arg Ala Thr Pro Leu Leu Gln Thr Ala Glu Ile Met Thr Pro Pro
228 35 40 45
230 act aag acc tta tgg ccc aag ggt tcc aac gcc agt ctg gcg cgg tcg 432
231 Thr Lys Thr Leu Trp Pro Lys Gly Ser Asn Ala Ser Leu Ala Arg Ser
232 50 55 60 65
234 ttg gca cct gcg gag gtg cct aaa gga gac agg acg gca gga tct ccg 480
235 Leu Ala Pro Ala Glu Val Pro Lys Gly Asp Arg Thr Ala Gly Ser Pro
236 70 75 80
238 cca cgc acc atc tcc cct ccc ccg tgc caa gga ccc atc gag atc aag 528
239 Pro Arg Thr Ile Ser Pro Pro Pro Cys Gln Gly Pro Ile Glu Ile Lys
240 85 90 95
242 gag act ttc aaa tac atc aac acg gtt gtg tcc tgc ctt gtg ttc gtg 576
243 Glu Thr Phe Lys Tyr Ile Asn Thr Val Val Ser Cys Leu Val Phe Val
244 100 105 110
246 ctg ggg atc atc ggg aac tcc aca ctt ctg aga att atc tac aag aac 624
247 Leu Gly Ile Ile Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lys Asn
248 115 120 125
250 aag tgc atg cga aac ggt ccc aat atc ttg atc gcc agc ttg gct ctg 672

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251	Lys	Cys	Met	Arg	Asn	Gly	Pro	Asn	Ile	Leu	Ile	Ala	Ser	Leu	Ala	Leu	
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254	gga	gac	ctg	ctg	cac	atc	gtc	att	gac	atc	cct	atc	aat	gtc	tac	aag	720
255	Gly	Asp	Leu	Leu	His	Ile	Val	Ile	Asp	Ile	Pro	Ile	Asn	Val	Tyr	Lys	
256					150					155					160		
258	ctg	ctg	gca	gag	gac	tgg	cca	ttt	gga	gct	gag	atg	tgt	aag	ctg	gtg	768
259	Leu	Leu	Ala	Glu	Asp	Trp	Pro	Phe	Gly	Ala	Glu	Met	Cys	Lys	Leu	Val	
260				165					170					175			
262	cct	ttc	ata	cag	aaa	gcc	tcc	gtg	gga	atc	act	gtg	ctg	agt	cta	tgt	816
263	Pro	Phe	Ile	Gln	Lys	Ala	Ser	Val	Gly	Ile	Thr	Val	Leu	Ser	Leu	Cys	
264			180					185					190				
266	gct	ctg	agt	att	gac	aga	tat	cga	gct	gtt	gct	tct	tgg	agt	aga	att	864
267	Ala	Leu	Ser	Ile	Asp	Arg	Tyr	Arg	Ala	Val	Ala	Ser	Trp	Ser	Arg	Ile	
268		195					200					205					
270	aaa	gga	att	ggg	gtt	cca	aaa	tgg	aca	gca	gta	gaa	att	gtt	ttg	att	912
271	Lys	Gly	Ile	Gly	Val	Pro	Lys	Trp	Thr	Ala	Val	Glu	Ile	Val	Leu	Ile	
272	210				215						220				225		
274	tgg	gtg	gtc	tct	gtg	gtt	ctg	gct	gtc	cct	gaa	gcc	ata	ggt	ttt	gat	960
275	Trp	Val	Val	Ser	Val	Val	Leu	Ala	Val	Pro	Glu	Ala	Ile	Gly	Phe	Asp	
276				230					235					240			
278	ata	att	acg	atg	gac	tac	aaa	gga	agt	tat	ctg	cga	atc	tgc	ttg	ctt	1008
279	Ile	Ile	Thr	Met	Asp	Tyr	Lys	Gly	Ser	Tyr	Leu	Arg	Ile	Cys	Leu	Leu	
280			245					250					255				
282	cat	ccc	gtt	cag	aag	aca	gct	ttc	atg	cag	ttt	tac	aag	aca	gca	aaa	1056
283	His	Pro	Val	Gln	Lys	Thr	Ala	Phe	Met	Gln	Phe	Tyr	Lys	Thr	Ala	Lys	
284			260					265					270				
286	gat	tgg	tgg	ctg	ttc	agt	ttc	tat	ttc	tgc	ttg	cca	ttg	gcc	atc	act	1104
287	Asp	Trp	Trp	Leu	Phe	Ser	Phe	Tyr	Phe	Cys	Leu	Pro	Leu	Ala	Ile	Thr	
288		275					280					285					
290	gca	ttt	ttt	tat	aca	cta	atg	acc	tgt	gaa	atg	ttg	aga	aag	aaa	agt	1152
291	Ala	Phe	Phe	Tyr	Thr	Leu	Met	Thr	Cys	Glu	Met	Leu	Arg	Lys	Lys	Ser	
292	290				295					300					305		
294	ggc	atg	cag	att	gct	tta	aat	gat	cac	cta	aag	cag	aga	cgg	gaa	gtg	1200
295	Gly	Met	Gln	Ile	Ala	Leu	Asn	Asp	His	Leu	Lys	Gln	Arg	Arg	Glu	Val	
296				310					315						320		
298	gcc	aaa	acc	gtc	ttt	tgc	ctg	gtc	ctt	gtc	ttt	gcc	ctc	tgc	tgg	ctt	1248
299	Ala	Lys	Thr	Val	Phe	Cys	Leu	Val	Leu	Val	Phe	Ala	Leu	Cys	Trp	Leu	
300			325					330					335				
302	ccc	ctt	cac	ctc	agc	agg	att	ctg	aag	ctc	act	ctt	tat	aat	cag	aat	1296
303	Pro	Leu	His	Leu	Ser	Arg	Ile	Leu	Lys	Leu	Thr	Leu	Tyr	Asn	Gln	Asn	
304			340					345					350				
306	gat	ccc	aat	aga	tgt	gaa	ctt	ttg	agc	ttt	ctg	ttg	gta	ttg	gac	tat	1344
307	Asp	Pro	Asn	Arg	Cys	Glu	Leu	Leu	Ser	Phe	Leu	Leu	Val	Leu	Asp	Tyr	
308		355				360				365							
310	att	ggt	atc	aac	atg	gct	tca	ctg	aat	tcc	tgc	att	aac	cca	att	gct	1392
311	Ile	Gly	Ile	Asn	Met	Ala	Ser	Leu	Asn	Ser	Cys	Ile	Asn	Pro	Ile	Ala	
312	370				375					380					385		
314	ctg	tat	ttg	gtg	agc	aaa	aga	ttc	aaa	aac	tgc	ttt	aag	tca	tgc	tta	1440
315	Leu	Tyr	Leu	Val	Ser	Lys	Arg	Phe	Lys	Asn	Cys	Phe	Lys	Ser	Cys	Leu	

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date